OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/044,205A

DATE: 05/02/2002
TIME: 16:31:06

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\05022002\J044205A.raw

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      3 <110> APPLICANT: KAPELLER-LIBERMANN, Rosana
      4       BANDARU, Rajasekhar
      6 <120> TITLE OF INVENTION: 69087, 15821, and 15418, Methods and Compositions of Human
Proteins and
      7       Uses Thereof
      9 <130> FILE REFERENCE: 10147-52U1
     11 <140> CURRENT APPLICATION NUMBER: 10/044,205A
C--> 12 <141> CURRENT FILING DATE: 2002-04-19
     14 <150> PRIOR APPLICATION NUMBER: US 60/242,428
     15 <151> PRIOR FILING DATE: 2000-10-23
     17 <150> PRIOR APPLICATION NUMBER: US 60/241,884
     18 <151> PRIOR FILING DATE: 2000-10-20
     20 <150> PRIOR APPLICATION NUMBER: US 60/241,877
     21 <151> PRIOR FILING DATE: 2000-10-20
     23 <160> NUMBER OF SEQ ID NOS: 44
     25 <170> SOFTWARE: PatentIn version 3.1
     27 <210> SEQ ID NO: 1
     28 <211> LENGTH: 2198
     29 <212> TYPE: DNA
     30 <213> ORGANISM: Homo sapiens
     32 <400> SEQUENCE: 1
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     37 gtcaaagctt cttacaaaag aaacctcttt cacaccctcc acgggtccca cccacaggcc    180
     39 acaggactca ctgtaaatcc cttggacgtt gtctcacccg ggaagggaaa gcagccagca    240
     41 gccctccagc cctcttgtgc tttccctggg agtgcgcccc gtgctcagcc atggtggaca    300
     43 tgggggccct ggacaacctg atcgccaaca ccgcctacct gcaggcccgg aagccctcgg    360
     45 actgcgacag caaagagctg cagcggcggc ggcgtagcct ggccctgccc gggctgcagg    420
     47 gctgcgcgga gctccgccag aagctgtccc tgaacttcca cagcctgtgt gagcagcagc    480
     49 ccatcggtcg ccgcctcttc cgtgacttcc tagccacagt gcccacgttc cgcaaggcgg    540
     51 caaccttcct agaggacgtg cagaactggg agctggccga ggagggaccc accaaagaca    600
     53 gcgcgctgca ggggctggtg gccacttgtg cgagtgcccc tgccccgggg aacccgcaac    660
     55 ccttcctcag ccaggccgtg gccaccaagt gccaagcagc caccactgag gaagagcgag    720
     57 tggctgcagt gacgctgcgc aaggctgagg ccatggcttt cttgcaagag cagcccttta    780
     59 aggatttcgt gaccagcgcc ttctacgaca agtttctgca gtggaaactc ttcgagatgc    840
     61 aaccagtgtc agacaagtac ttcactgagt tcagagtgct ggggaaaggt ggttttgggg    900
     63 aggtatgtgc cgtccaggtg aaaaacactg ggaagatgta tgcctgtaag aaactggaca    960
     65 agaagcggct gaagaagaaa ggtggcgaga agatggctct cttggaaaag gaaatcttgg   1020
     67 agaaggtcag cagccctttc attgtctctc tggcctatgc ctttgagagc aagacccatc   1080
     69 tctgccttgt catgagcctg atgaatgggg gagacctcaa gttccacatc tacaacgtgg   1140
     71 gcacgcgtgg cctggacatg agccgggtga tcttttactc ggcccagata gcctgtggga   1200
     73 tgctgcacct ccatgaactc ggcatcgtct atcgggacat gaagcctgag aatgtgcttc   1260
     75 tggatgacct cggcaactgc aggttatctg acctggggct ggccgtggag atgaagggtg   1320
     77 gcaagcccat cacccagagg gctggaacca atggttacat ggctcctgag atcctaatgg   1380
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79 aaaaggtaag ttattcctat cctgtggact ggtttgccat gggatgcagc atttatgaaa   1440
81 tggttgctgg acgaacacca ttcaaagatt acaaggaaaa ggtcagtaaa gaggatctga   1500
83 agcaaagaac tctgcaagac gaggtcaaat tccagcatga taacttcaca gaggaagcaa   1560
85 aagatatttg caggctcttc ttggctaaga aaccagagca acgcttagga agcagagaaa   1620
87 agtctgatga tcccaggaaa catcatttct ttaaaacgat caactttcct cgcctggaag   1680
89 ctggcctaat tgaaccccca tttgtgccag acccttcagt ggtttatgcc aaagacatcg   1740
91 ctgaaattga tgatttctct gaggttcggg gggtggaatt tgatgacaaa gataagcagt   1800
93 tcttcaaaaa ctttgcgaca ggtgctgttc ctatagcatg gcaggaagaa attatagaaa   1860
95 cgggactgtt tgaggaactg aatgacccca acagacctac gggttgtgag gagggtaatt   1920
97 catccaagtc tggcgtgtgt ttgttattgt aaattgctct ctttaccaga caggcagcag   1980
99 gagtctcggc tgacataatc ctcgaatgtt ccacacgtgg aaatctgtgg aatgagggct   2040
101 aatcagttag gagggacatc acaaccacaa aacaattcaa aagacaggca agctcactac   2100
103 tagaacacat tttattttct ttttctttct tcataaagat gagtaaagtc tcagttttca   2160
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109 <211> LENGTH: 553
110 <212> TYPE: PRT
111 <213> ORGANISM: Homo sapiens
113 <400> SEQUENCE: 2
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120             20                  25                  30
123 Arg Arg Arg Ser Leu Ala Leu Pro Gly Leu Gln Gly Cys Ala Glu Leu
124         35                  40                  45
127 Arg Gln Lys Leu Ser Leu Asn Phe His Ser Leu Cys Glu Gln Gln Pro
128     50                  55                  60
131 Ile Gly Arg Arg Leu Phe Arg Asp Phe Leu Ala Thr Val Pro Thr Phe
132 65                  70                  75                  80
135 Arg Lys Ala Ala Thr Phe Leu Glu Asp Val Gln Asn Trp Glu Leu Ala
136                 85                  90                  95
139 Glu Glu Gly Pro Thr Lys Asp Ser Ala Leu Gln Gly Leu Val Ala Thr
140             100                 105                 110
143 Cys Ala Ser Ala Pro Ala Pro Gly Asn Pro Gln Pro Phe Leu Ser Gln
144         115                 120                 125
147 Ala Val Ala Thr Lys Cys Gln Ala Ala Thr Thr Glu Glu Glu Arg Val
148     130                 135                 140
151 Ala Ala Val Thr Leu Arg Lys Ala Glu Ala Met Ala Phe Leu Gln Glu
152 145                 150                 155                 160
155 Gln Pro Phe Lys Asp Phe Val Thr Ser Ala Phe Tyr Asp Lys Phe Leu
156                 165                 170                 175
159 Gln Trp Lys Leu Phe Glu Met Gln Pro Val Ser Asp Lys Tyr Phe Thr
160             180                 185                 190
163 Glu Phe Arg Val Leu Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Val
164         195                 200                 205
167 Gln Val Lys Asn Thr Gly Lys Met Tyr Ala Cys Lys Lys Leu Asp Lys
168     210                 215                 220
171 Lys Arg Leu Lys Lys Lys Gly Gly Glu Lys Met Ala Leu Leu Glu Lys
172 225                 230                 235                 240
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Input Set : A:\pto.vsk.txt
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```
175 Glu Ile Leu Glu Lys Val Ser Ser Pro Phe Ile Val Ser Leu Ala Tyr
176                 245                 250                 255
179 Ala Phe Glu Ser Lys Thr His Leu Cys Leu Val Met Ser Leu Met Asn
180             260                 265                 270
183 Gly Gly Asp Leu Lys Phe His Ile Tyr Asn Val Gly Thr Arg Gly Leu
184         275                 280                 285
187 Asp Met Ser Arg Val Ile Phe Tyr Ser Ala Gln Ile Ala Cys Gly Met
188     290                 295                 300
191 Leu His Leu His Glu Leu Gly Ile Val Tyr Arg Asp Met Lys Pro Glu
192 305                 310                 315                 320
195 Asn Val Leu Leu Asp Asp Leu Gly Asn Cys Arg Leu Ser Asp Leu Gly
196                 325                 330                 335
199 Leu Ala Val Glu Met Lys Gly Gly Lys Pro Ile Thr Gln Arg Ala Gly
200             340                 345                 350
203 Thr Asn Gly Tyr Met Ala Pro Glu Ile Leu Met Glu Lys Val Ser Tyr
204         355                 360                 365
207 Ser Tyr Pro Val Asp Trp Phe Ala Met Gly Cys Ser Ile Tyr Glu Met
208     370                 375                 380
211 Val Ala Gly Arg Thr Pro Phe Lys Asp Tyr Lys Glu Lys Val Ser Lys
212 385                 390                 395                 400
215 Glu Asp Leu Lys Gln Arg Thr Leu Gln Asp Glu Val Lys Phe Gln His
216                 405                 410                 415
219 Asp Asn Phe Thr Glu Glu Ala Lys Asp Ile Cys Arg Leu Phe Leu Ala
220             420                 425                 430
223 Lys Lys Pro Glu Gln Arg Leu Gly Ser Arg Glu Lys Ser Asp Asp Pro
224         435                 440                 445
227 Arg Lys His His Phe Phe Lys Thr Ile Asn Phe Pro Arg Leu Glu Ala
228     450                 455                 460
231 Gly Leu Ile Glu Pro Pro Phe Val Pro Asp Pro Ser Val Val Tyr Ala
232 465                 470                 475                 480
235 Lys Asp Ile Ala Glu Ile Asp Asp Phe Ser Glu Val Arg Gly Val Glu
236                 485                 490                 495
239 Phe Asp Asp Lys Asp Lys Gln Phe Phe Lys Asn Phe Ala Thr Gly Ala
240             500                 505                 510
243 Val Pro Ile Ala Trp Gln Glu Glu Ile Ile Glu Thr Gly Leu Phe Glu
244         515                 520                 525
247 Glu Leu Asn Asp Pro Asn Arg Pro Thr Gly Cys Glu Glu Gly Asn Ser
248     530                 535                 540
251 Ser Lys Ser Gly Val Cys Leu Leu Leu
252 545                 550
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256 <211> LENGTH: 1659
257 <212> TYPE: DNA
258 <213> ORGANISM: Homo sapiens
260 <400> SEQUENCE: 3
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263 aagccctcgg actgcgacag caaagagctg cagcggcggc ggcgtagcct ggccctgccc    120
265 gggctgcagg gctgcgcgga gctccgccag aagctgtccc tgaacttcca cagcctgtgt    180
267 gagcagcagc ccatcggtcg ccgcctcttc cgtgacttcc tagccacagt gcccacgttc    240
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PATENT APPLICATION: US/10/044,205A TIME: 16:31:06

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     269 cgcaaggcgg caaccttcct agaggacgtg cagaactggg agctggccga ggagggaccc    300
     271 accaaagaca gcgcgctgca ggggctggtg gccacttgtg cgagtgcccc tgccccgggg    360
     273 aacccgcaac ccttcctcag ccaggccgtg gccaccaagt gccaagcagc caccactgag    420
     275 gaagagcgag tggctgcagt gacgctgcgc aaggctgagg ccatggcttt cttgcaagag    480
     277 cagcccttta aggatttcgt gaccagcgcc ttctacgaca agtttctgca gtggaaactc    540
     279 ttcgagatgc aaccagtgtc agacaagtac ttcactgagt tcagagtgct ggggaaaggt    600
     281 ggttttgggg aggtatgtgc cgtccaggtg aaaaacactg ggaagatgta tgcctgtaag    660
     283 aaactggaca agaagcggct gaagaagaaa ggtggcgaga agatggctct cttggaaaag    720
     285 gaaatcttgg agaaggtcag cagcctttc attgtctctc tggcctatgc ctttgagagc    780
     287 aagacccatc tctgccttgt catgagcctg atgaatgggg gagacctcaa gttccacatc    840
     289 tacaacgtgg gcacgcgtgg cctggacatg agccgggtga tcttttactc ggcccagata    900
     291 gcctgtggga tgctgcacct ccatgaactc ggcatcgtct atcgggacat gaagcctgag    960
     293 aatgtgcttc tggatgacct cggcaactgc aggttatctg acctggggct ggccgtggag   1020
     295 atgaagggtg gcaagcccat cacccagagg gctggaacca atggttacat ggctcctgag   1080
     297 atcctaatgg aaaaggtaag ttattcctat cctgtggact ggtttgccat gggatgcagc   1140
     299 atttatgaaa tggttgctgg acgaacacca ttcaaagatt acaaggaaaa ggtcagtaaa   1200
     301 gaggatctga agcaaagaac tctgcaagac gaggtcaaat tccagcatga taacttcaca   1260
     303 gaggaagcaa aagatatttg caggctcttc ttggctaaga aaccagagca acgcttagga   1320
     305 agcagagaaa agtctgatga tcccaggaaa catcatttct ttaaaacgat caactttcct   1380
     307 cgcctggaag ctggcctaat tgaaccccca tttgtgccag acccttcagt ggtttatgcc   1440
     309 aaagacatcg ctgaaattga tgatttctct gaggttcggg gggtggaatt tgatgacaaa   1500
     311 gataagcagt tcttcaaaaa ctttgcgaca ggtgctgttc ctatagcatg gcaggaagaa   1560
     313 attatagaaa cgggactgtt tgaggaactg aatgacccca acagacctac gggttgtgag   1620
     315 gagggtaatt catccaagtc tggcgtgtgt ttgttattg                         1659
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     319 <211> LENGTH: 0
     320 <212> TYPE: DNA
     321 <213> ORGANISM: Homo sapiens
     323 <400> SEQUENCE: 4
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     326 <210> SEQ ID NO: 5
     327 <211> LENGTH: 0
     328 <212> TYPE: DNA
     329 <213> ORGANISM: Homo sapiens
     331 <400> SEQUENCE: 5
W--> 332 000
     334 <210> SEQ ID NO: 6
     335 <211> LENGTH: 0
     336 <212> TYPE: DNA
     337 <213> ORGANISM: Homo sapiens
     339 <400> SEQUENCE: 6
W--> 340 000
     342 <210> SEQ ID NO: 7
     343 <211> LENGTH: 0
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W--> 348 000
     350 <210> SEQ ID NO: 8
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PATENT APPLICATION: US/10/044,205A TIME: 16:31:06

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\05022002\J044205A.raw

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     352 <212> TYPE: DNA
     353 <213> ORGANISM: Homo sapiens
     355 <400> SEQUENCE: 8
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     359 <211> LENGTH: 0
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     361 <213> ORGANISM: Homo sapiens
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     366 <210> SEQ ID NO: 10
     367 <211> LENGTH: 0
     368 <212> TYPE: DNA
     369 <213> ORGANISM: Homo sapiens
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W--> 372 000
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     375 <211> LENGTH: 553
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     377 <213> ORGANISM: Homo sapiens
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     385 Leu Gln Ala Arg Lys Pro Ser Asp Cys Asp Ser Lys Glu Leu Gln Arg
     386             20                  25                  30
     389 Arg Arg Arg Ser Leu Ala Leu Pro Gly Leu Gln Gly Cys Ala Glu Leu
     390         35                  40                  45
     393 Arg Gln Lys Leu Ser Leu Asn Phe His Ser Leu Cys Glu Gln Gln Pro
     394     50                  55                  60
     397 Ile Gly Arg Arg Leu Phe Arg Asp Phe Leu Ala Thr Val Pro Thr Phe
     398 65                  70                  75                  80
     401 Arg Lys Ala Ala Thr Phe Leu Glu Asp Val Gln Asn Trp Glu Leu Ala
     402                 85                  90                  95
     405 Glu Glu Gly Pro Thr Lys Asp Ser Ala Leu Gln Gly Leu Val Ala Thr
     406             100                 105                 110
     409 Cys Ala Ser Ala Pro Ala Pro Gly Asn Pro Gln Pro Phe Leu Ser Gln
     410         115                 120                 125
     413 Ala Val Ala Thr Lys Cys Gln Ala Ala Thr Thr Glu Glu Glu Arg Val
     414     130                 135                 140
     417 Ala Ala Val Thr Leu Ala Lys Ala Glu Ala Met Ala Phe Leu Gln Glu
     418 145                 150                 155                 160
     421 Gln Pro Phe Lys Asp Phe Val Thr Ser Ala Phe Tyr Asp Lys Phe Leu
     422                 165                 170                 175
     425 Gln Trp Lys Leu Phe Glu Met Gln Pro Val Ser Asp Lys Tyr Phe Thr
     426             180                 185                 190
     429 Glu Phe Arg Val Leu Gly Lys Gly Gly Phe Gly Glu Val Cys Ala Val
     430         195                 200                 205
     433 Gln Val Lys Asn Thr Gly Lys Met Tyr Ala Cys Lys Lys Leu Asp Lys
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/02/2002
PATENT APPLICATION: US/10/044,205A TIME: 16:31:07

Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\05022002\J044205A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:33; Xaa Pos. 31,38

VERIFICATION SUMMARY DATE: 05/02/2002
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Input Set : A:\pto.vsk.txt
Output Set: N:\CRF3\05022002\J044205A.raw

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:324 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (4) SEQUENCE:
L:332 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (5) SEQUENCE:
L:340 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (6) SEQUENCE:
L:348 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:356 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:364 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (9) SEQUENCE:
L:372 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (10) SEQUENCE:
L:968 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (15) SEQUENCE:
L:976 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (16) SEQUENCE:
L:984 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (17) SEQUENCE:
L:992 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (18) SEQUENCE:
L:1000 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (19) SEQUENCE:
L:1008 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (20) SEQUENCE:
L:1341 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (24) SEQUENCE:
L:1349 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (25) SEQUENCE:
L:1357 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (26) SEQUENCE:
L:1365 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (27) SEQUENCE:
L:1373 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (28) SEQUENCE:
L:1381 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (29) SEQUENCE:
L:1389 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (30) SEQUENCE:
L:1812 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:16
L:1816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:32
L:2039 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (37) SEQUENCE:
L:2047 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (38) SEQUENCE:
L:2055 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (39) SEQUENCE:
L:2063 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (40) SEQUENCE: